

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2001, 13:44:05 ; Search time 10.66 Seconds  
(without alignments)  
1693.494 Million cell updates/sec

Title: US-09-784-340-2

Sequence: 1 MSRSKSNALVFLLLQLPCVGC.....KCFLFSCQKFNKTRKIKRE 527

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	7.6	527	1	UDAL_RAT
2	33	6.3	528	1	UDB4_HUMAN
3	33	6.3	530	1	UDBH_HUMAN
4	30	5.7	528	1	UDBJ_MACFA
5	29	5.5	529	1	UDBI_RAT
6	28	5.3	528	1	UDBA_HUMAN
7	28	5.3	529	1	UDB7_HUMAN
8	28	5.3	529	1	UDB9_HUMAN
9	24	4.6	530	1	UDBC_RAT
10	23	4.4	530	1	UDBE_RAT
11	23	4.4	530	1	UDBF_HUMAN
12	23	4.4	530	1	UDBG_MACFA
13	21	4.0	531	1	UDBD_RABIT
14	19	3.6	502	1	UDCI_RABIT
15	19	3.6	529	1	UDBR_HUMAN
16	18	3.4	530	1	UDBE_RAT
17	18	3.4	530	1	UDBE_RABIT
18	17	3.2	530	1	UDBE_MOUSE
19	16	3.0	523	1	UDBG_MOUSE
20	14	2.7	530	1	UDBE_RAT
21	14	2.7	530	1	UDBE_RAT
22	11	2.1	531	1	UDBE_MOUSE
23	11	2.1	533	1	UDBE_MOUSE
24	10	1.9	529	1	UDBE_RAT
25	10	1.9	530	1	UDBE_RAT
26	10	1.9	531	1	UDBE_RAT
27	10	1.9	531	1	UDBE_RAT
28	10	1.9	531	1	UDBE_RAT
29	10	1.9	533	1	UDBE_RAT
30	10	1.9	535	1	UDBE_RAT
31	9	1.7	530	1	UDBE_MOUSE
32	9	1.7	530	1	UDBE_MOUSE
33	9	1.7	531	1	UDBE_MOUSE

34	9	1.7	531	1	UDBE_RABIT	028611 oryctolagus
35	9	1.7	532	1	UDBE_RABIT	028612 oryctolagus
36	9	1.7	533	1	UDBE_HUMAN	P22309 homo sapien
37	9	1.7	534	1	UDBE_HUMAN	P35503 homo sapien
38	9	1.7	534	1	UDBE_HUMAN	P22310 homo sapien
39	9	1.7	534	1	UDBE_HUMAN	P35504 homo sapien
40	9	1.7	535	1	UDBE_MOUSE	063886 mus musculu
41	8	1.5	98	1	PER_BURFI	P13106 bunnillieriop
42	8	1.5	515	1	HEMI_CLOVO	059292 clostridium
43	8	1.5	541	1	CGT_HUMAN	016880 homo sapien
44	8	1.5	541	1	CGT_MOUSE	064676 mus musculu
45	8	1.5	541	1	CGT_RAT	009426 rattus norv

## ALIGNMENTS

RESULT	ID	UDAL_RAT	STANDARD	PRT	527 AA.
AC	P36510	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	UDP-GLUCURONOSYLTRANSFERASE 2A1 PRECURSOR, MICROSOAL (EC 2.4.1.17)				
DE	(UDPRT) (UGT-OLP)				
GN	UGT2A1 OR UGT2A-1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91156050; PubMed=1900353;				
RA	Lazard D., Zupko K., Porta Y., Nef P., Lazarevics J., Horn S.,				
RA	Khen M., Lancel D.;				
RT	Odorant signal termination by olfactory UDP glucuronosyl				
RT	transferase.;				
RL	Nature 349:790-793(1991).				
CC	-1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND				
CC	SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND				
CC	ENDOGENOUS COMPOUNDS. THIS ISOMER IS ACTIVE ON ODORANTS AND				
CC	SEEMS TO BE INVOLVED IN OLFACTION. IT COULD HELP CLEAR LIPOPHILIC				
CC	ODORANT MOLECULES FROM THE SENSORY EPITHELIUM.				
CC	-1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR				
CC	BETA-D-GLUCURONOSIDE.				
CC	-1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.				
CC	-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: X57565; NOT ANNOTATED. CDS.				
DR	InterPro: IPR002213; .				
DR	PFam: PF00201; UDPGT: 1.				
DR	PROSITE: PS00375; UDPGT: 1.				
KW	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;				
KW	Multigene family; Microsome; Olfaction.				
FT	SIGNAL	1	20	POTENTIAL.	
FT	CHAIN	21	527	UDP-GLUCURONOSYLTRANSFERASE 2A1.	
FT	TRANSMEM	491	507	POTENTIAL.	
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	313	313	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	527 AA;	59915 MW;	6A32A9B56EB8E8DE CRC64;	

Query Match 7.6%; Score 40; DB 1; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3.8e-33;

Need  
NA search.

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 436 YKENAMRLSRHHDPVKPLDRAVFWIEFWVRHKGAKHLR 475  
 Db 436 YKENAMRLSRHHDPVKPLDRAVFWIEFWVRHKGAKHLR 475

RESULT 2  
 ID UDB4\_HUMAN STANDARD; PRT; 528 AA.  
 AC P06133; P36538; 060731; 060867;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
 GN (UDPCT) (HYDROXYCHOLIC ACID) (HUC25) (UDPCH-1).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87241362; PubMed=3109396;  
 RA Jackson M.R., McCarthy L.R., Harding D., Wilson S., Coughtrie M.W.H.,  
 RA Burchell B.;  
 RT "Cloning of a human liver microsomal UDP-glucuronosyltransferase  
 RT cDNA.";  
 RL Biochem. J. 242:581-588(1987).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93326164; PubMed=8333863;  
 RA Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;  
 RT "cDNA cloning and expression of two new members of the human liver  
 RT UDP-glucuronosyltransferase 2B subfamily.";  
 RL Biochem. Biophys. Res. Commun. 194:436-503(1993).  
 RN (3)  
 RP SEQUENCE FROM N.A., AND VARIANT GIU-458.  
 RA Levesque E., Beaulieu M., Belanger A.;  
 RT "UGT2B4(E458): a UDP-glucuronosyltransferase encoded by a polymorphic  
 RT gene with differential substrate specificity.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. ACTIVE ON POLYHYDROXYLATED ESTROGENS (SUCH  
 CC AS ESTRADIOL, 4-HYDROXYESTRONE AND 2-HYDROXYESTRADIOL) AND XENOBIOTICS  
 CC (SUCH AS 4-METHYLBELBEPHENOL, 1-NAPHTHOL, 4-NITROPHENOL,  
 CC 2-AMINOPHENOL, 4-HYDROXYBIPHENYL AND MENTHOL).  
 CC -1- FUNCTION: CAPABLE OF 6 ALPHA-HYDROXYGLUCURONIDATION OF  
 CC HYDROXYCHOLIC ACID.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -1- CAUTION: REF. 2 THOUGHT THAT THIS WAS A NEW FORM (UGT2B11). THE  
 CC NAME UGT2B11 HAS NOW BEEN REUSED FOR ANOTHER HUMAN ENZYME.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL: Y00317; CA68415.1; -  
 CC EMBL: AF064200; AAC95002.1; -  
 CC EMBL: AJ005162; CA06396.1; -  
 CC PIR: A27878; A27878.  
 CC PIR: JN0619; JN0619.  
 CC MIM: 600067; -

DR InterPro; IPR002213; -  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Polymorphism.  
 FT SIGNAL 1 23  
 FT CHAIN 24 528  
 FT TRANSMEM 493 509  
 FT CARBOHYD 315 315  
 FT VARIANT 458 458  
 FT FT  
 FT CONFLICT 109 109  
 FT CONFLICT 171 172  
 FT CONFLICT 382 387  
 FT CONFLICT 396 396  
 FT SEQUENCE 528 AA; 60512 MW; 6B45B6769971A078 CRC64;

Query Match 6.38; Score 33; DB 1; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-26;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 443 LSRIHHDPVKPLDRAVFWIEFWVRHKGAKHLR 475  
 Db 445 LSRIHHDPVKPLDRAVFWIEFWVRHKGAKHLR 477

RESULT 3  
 ID UDB4\_HUMAN STANDARD; PRT; 530 AA.  
 AC 075795;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B17 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
 GN (UDPCT) (C19-STEROID SPECIFIC UDP-GLUCURONOSYLTRANSFERASE).  
 RN UGT2B17.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=96394358; PubMed=8798464;  
 RA Beaulieu M., Levesque E., Hum D.W., Belanger A.;  
 RT "Isolation and characterization of a novel cDNA encoding a human  
 RT UDP-glucuronosyltransferase active on C19 steroids.";  
 RL J. Biol. Chem. 271:22855-22862(1996).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98030207; PubMed=9364925;  
 RA Beaulieu M., Levesque E., Tchertouf A., Beatty B.G., Belanger A.,  
 RA Hum D.W.;  
 RT "Chromosomal localization, structure, and regulation of the UGT2B17  
 RT gene, encoding a C19 steroid metabolizing enzyme.";  
 RL DNA Cell Biol. 16:1143-1154(1997).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. THE MAJOR SUBSTRATES OF THIS ISOZYME ARE  
 CC ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >  
 CC ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >  
 CC ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES INCLUDING THE  
 CC LIVER, KIDNEY, TESTIS, UTERUS, PLACENTA, MAMMARY GLAND, ADRENAL  
 CC GLAND, SKIN, AND PROSTATE.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U59209; AAC25491.1; -  
DR MIM: 601903; -  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferrase: Glycosyltransferase; glycoprotein; Transmembrane; Signal;  
KM Multigene family; Microsome.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 1 530 UDP-GLUCURONOSYLTRANSFERASE 2B17.  
FT TRANSMEM 495 515 POTENTIAL.  
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 530 AA; 61095 MW; 8E59EBC43CE43760 CRC64;  
  
Query Match 6.3%; Score 33; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 6.5e-26;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 443 LSRHHDPYKPLDRAVFWIEFVNRHKGAKHLR 475  
DB 446 LSRHHDPYKPLDRAVFWIEFVNRHKGAKHLR 478  
|||||  
  
RESULT 4  
ID UDB1\_MACFA STANDARD; PRT; 528 AA.  
AC 09XN55;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B19 PRECURSOR, MICROSOMAL (EC 2.4.1.17).  
GN UGT2B19.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver, and Prostate;  
RX MEDLINE=99203465; PubMed=10102998;  
RA Belanger G., Barbier O., Hum D.W., Belanger A.;  
RT "Molecular cloning, expression and characterization of a monkey  
RT steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates  
RT testosterone";  
RN Eur. J. Biochem. 260:701-708(1999).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD  
CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES: EUGENOL, 4-  
CC METHYLBELBELIFERONE, P-NITROPHENOL, 1-NAPHTHOL, P,P'-BIPHENOL,  
CC NARINGENIN AND O,O'-BIPHENOL. ACTIVE ALSO ON 3A-HYDROXY AND 17B-  
CC HYDROXY POSITIONS OF STEROIDS.  
CC -1- FUNCTION: CONTRIBUTES TO THE FORMATION OF ANDROGEN GLUCURONIDE IN  
CC EXTRAHEPATIC STEROID TARGET TISSUES SUCH AS THE PROSTATE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, OVARY, PROSTATE, COLON,  
CC KIDNEY, PANCREAS, BRAIN, CEREBELLUM, MAMMARY GLAND AND EPIDIDYMS.  
CC NOT EXPRESSED IN SMALL INTESTINE, SPLEEN, BLADDER, ADRENAL GLAND  
CC AND TESTIS.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF112112; AAD24435.1; -  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferrase: Glycosyltransferase; glycoprotein; Transmembrane; Signal;  
KM Multigene family; Microsome.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 1 528 UDP-GLUCURONOSYLTRANSFERASE 2B19.  
FT TRANSMEM 493 513 POTENTIAL.  
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 528 AA; 60741 MW; 3BFD2AE714A27AEE CRC64;  
  
Query Match 5.7%; Score 30; DB 1; Length 528;  
Best Local Similarity 100.0%; Pred. No. 8.2e-23;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 446 IHHDQPYKPLDRAVFWIEFVNRHKGAKHLR 475  
DB 448 IHHDQPYKPLDRAVFWIEFVNRHKGAKHLR 477  
|||||  
  
RESULT 5  
ID UDB1\_RAT STANDARD; PRT; 529 AA.  
AC P09875;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-JUN-1999 (Rel. 38, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPGT) (UDPGTR-2).  
GN UGT2B1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86196018; PubMed=3084479;  
RA McKenzie P.I.;  
RT "Rat liver UDP-glucuronosyltransferase. Sequence and expression of a  
RT cDNA encoding a phenobarbital-inducible form";  
RN J. Biol. Chem. 261:6119-6125(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90293083; PubMed=2113533;  
RA McKenzie P.I., Rodboun L.;  
RT "Organization of the rat UDP-glucuronosyltransferase, UDPGTR-2, gene  
RT and characterization of its promoter";  
RN J. Biol. Chem. 265:11328-11332(1990).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- INDUCTION: BY PHENOBARBITAL.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC EMBL: M13506; AAA42313.1; -  
 DR EMBL: M35086; AAA42310.1; -  
 DR EMBL: M35202; AAA42310.1; JOINED.  
 DR EMBL: M35080; AAA42310.1; JOINED.  
 DR EMBL: M35082; AAA42310.1; JOINED.  
 DR EMBL: M35083; AAA42310.1; JOINED.  
 DR PIR: A24324; A24324.  
 DR PIR: A24233; A24233.  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT.1  
 DR PROSITE: PS00375; UDPGT.1  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KM Multigene family; Microsome.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 529 UDP-GLUCURONOSYLTRANSFERASE 2B1.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA: 60484 MW: 14DF0224BFC3044 CRC64;

Query Match 5.5%; Score 29; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-22;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 435 SYKNAARLSRIHDDQPKPLDRAVFWIE 463  
 DB 438 SYKNAARLSRIHDDQPKPLDRAVFWIE 466

RESULT 6  
 UDBA HUMAN STANDARD; PRT; 528 AA.  
 AC P36537;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B10 PRECURSOR, MICROSMAL (EC 2.4.1.17) (UDPGT).  
 GN UGT2B10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93326164; PubMed=8333863;  
 RA Jin G.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;  
 RT "cDNA cloning and expression of two new members of the human liver  
 UDP-glucuronosyltransferase 2B subfamily";  
 RT Biochem. Biophys. Res. Commun. 194:496-503(1993).  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 BETA-D-GLUCONOSIDE.  
 CC -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X63359; CAA44961.1; -  
 DR PIR: JN0620; JN0620.  
 DR MIM: 600070; -

DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT.1  
 DR PROSITE: PS00375; UDPGT.1  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KM Multigene family; Microsome.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 528 UDP-GLUCURONOSYLTRANSFERASE 2B10.  
 FT TRANSMEM 492 512 POTENTIAL.  
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 528 AA: 60774 MW: 5E6EA3DEC032C2E0 CRC64;

Query Match 5.3%; Score 28; DB 1; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-21;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDQPKPLDRAVFWIEFVRRHKGAKHLR 475  
 DB 449 HDQPKPLDRAVFWIEFVRRHKGAKHLR 476

RESULT 7  
 UDB7 HUMAN STANDARD; PRT; 529 AA.  
 AC P16662;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B7 PRECURSOR, MICROSMAL (EC 2.4.1.17) (UDPGT) (3,4-CATECHOL ESTROGEN SPECIFIC) (UDPETH-2).  
 GN UGT2B7 OR UGT2B9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90243659; PubMed=2159463;  
 RA Ritter J.K., Sheen Y.Y., Owens I.S.;  
 RT "Cloning and expression of human liver UDP-glucuronosyltransferase in  
 COS-1 cells. 3,4-catechol estrogens and estril as primary  
 RT substrates";  
 RT J. Biol. Chem. 265:7900-7906(1990)  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -!- FUNCTION: ITS UNIQUE SPECIFICITY FOR 3,4-CATECHOL ESTROGENS AND  
 ESTRIOL SUGGESTS IT MAY PLAY AN IMPORTANT ROLE IN REGULATING THE  
 LEVEL AND ACTIVITY OF THESE POTENT AND ACTIVE ESTROGEN  
 METABOLITES.  
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 BETA-D-GLUCONOSIDE.  
 CC -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: J05428; AAA36793.1; -  
 DR PIR: A35366; A35366.  
 DR MIM: 600068; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT.1  
 DR PROSITE: PS00375; UDPGT.1  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;

KM Multigene family: Microsome.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 529 UDP-GLUCURONOSYLTRANSFERASE 2B7.  
 FT TRANSMEM 493 509 POTENTIAL.  
 FT CAROHND 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHND 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHND 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA: 60694 MW: 9481CA6CE92F1446 CRC64;

Query Match 5.3%; Score 28; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-21;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDQPVKPLDRAVWIEFVNRHGAKHLR 475  
 DB 450 HDQPVKPLDRAVWIEFVNRHGAKHLR 477

RESULT 8  
 UDB9\_MACFA STANDARD; PRT; 529 AA.  
 AC 002663;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B9 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT).  
 GN UGT2B9.  
 OS Maccaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 RX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RC MEDLINE=98030212; PubMed=9364930;  
 RA Belanger G., Beaulieu M., Levesque E., Hum D.W., Belanger A.;  
 RT "Expression and characterization of a novel  
 RT UDP-glucuronosyltransferase, UGT2B9, from cynomolgus monkey.";  
 RT DNA Cell Biol. 16:1195-1205(1997).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME IS ACTIVE ON C18, C19, AND C21  
 CC STEROIDS, BILE ACIDS, AND SEVERAL XENOBIOTICS INCLUDING EUGENOL,  
 CC 1-NAPHTHOL, AND P-NITROPHENOL.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U91582; AAB50249.1; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT; 1.  
 DR PROSITE: PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 2 BY SIMILARITY.  
 FT CHAIN 1 529 UDP-GLUCURONOSYLTRANSFERASE 2B9.  
 FT TRANSMEM 494 514 POTENTIAL.  
 FT CAROHND 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHND 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHND 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA: 60970 MW: F110F85FE3A9B8D CRC64;

Query Match 5.3%; Score 28; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-21;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDQPVKPLDRAVWIEFVNRHGAKHLR 475  
 DB 450 HDQPVKPLDRAVWIEFVNRHGAKHLR 477

RESULT 9  
 UDB9\_MACFA STANDARD; PRT; 530 AA.  
 AC 002663;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B12 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT).  
 GN UGT2B12.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver, and Kidney;  
 RC MEDLINE=96032669; PubMed=7574722;  
 RA Green M.D., Clarke D.J., Oturu E.M., Styczynski P.B.,  
 RA Jackson M.R., Burchell B., Teply T.R.;  
 RT "Cloning and expression of a rat liver phenobarbital-inducible UDP-  
 RT glucuronosyltransferase (2B12) with specificity for monoterpenoid  
 RT alcohols.";  
 RT Arch. Biochem. Biophys. 322:460-468(1995).  
 RN [2]  
 RP SEQUENCE OF 24-38. AND CHARACTERIZATION.  
 RC STRAIN=MISTAR; TISSUE=Liver;  
 RC MEDLINE=9131237; PubMed=1906977;  
 RA Styczynski P.B., Green M.S., Pulg J., Coffman B.L., Teply T.R.;  
 RT "Purification and properties of a rat liver phenobarbital-inducible  
 RT 4-hydroxyphenyl UDP-glucuronosyltransferase.";  
 RT Mol. Pharmacol. 40:80-84(1991).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. CATALYZES THE TRANSFER OF GLUCURONIC ACID  
 CC FROM UDP-GLUCURONIC ACID TO VARIOUS AGLYCONE MOLECULES. CATALYZES  
 CC THE GLUCURONIDATION OF MONOTERPENOID ALCOHOLS, SUCH AS (-)-  
 CC BORNEOL, (+)-MENTHOL, AND (-)-NOROL. IN ADDITION, A NUMBER OF  
 CC SIMPLE PHENOLIC COMPOUNDS, SUCH AS HYDROXYBIPHENYLS, 7-  
 CC HYDROXYLATED COUMARINS, P-NITROPHENOL, AND FOOD-DERIVED SUBSTANCES  
 CC (E.G., NARINGENIN AND EUGENOL), AND 4-METHYLBELBILFERONE ARE ALSO  
 CC SUBSTRATES.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS SEEN IN THE KIDNEY AND  
 CC TESTIS.  
 CC -1- INDUCTION: BY PHENOBARBITAL.  
 CC -1- PTM: N-GLYCOSYLATED (PROBABLE).  
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE LIVER ISOZYME.  
 CC -1- THE KIDNEY ISOFORMS DIFFERS IN 12 POSITIONS.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U06273; AAB3404.1; -

DR EMBL: U06274; AAA83405.1; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPCT: 1.  
 DR PROSITE: PS00375; UDPCT: 1.  
 KM Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 23  
 FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B12.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC.. ) (POTENTIAL).  
 FT VARIANT 2 2 S -> P (IN KIDNEY).  
 FT VARIANT 61 61 F -> S (IN KIDNEY).  
 FT VARIANT 71 71 D -> H (IN KIDNEY).  
 FT VARIANT 95 95 N -> S (IN KIDNEY).  
 FT VARIANT 183 183 Q -> K (IN KIDNEY).  
 FT VARIANT 346 346 P -> T (IN KIDNEY).  
 FT VARIANT 398 398 A -> G (IN KIDNEY).  
 FT VARIANT 414 415 VE -> AT (IN KIDNEY).  
 FT VARIANT 433 433 V -> D (IN KIDNEY).  
 FT VARIANT 475 475 K -> L (IN KIDNEY).  
 FT VARIANT 488 488 K -> L (IN KIDNEY).  
 SQ SEQUENCE 530 AA; 61060 MW; D49313CE3E6D5BFD CRC64;

Query Match 4.6%; Score 24; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 453 KPLDRAVWIEFWYMRHKGAKHLRS 476  
 Db 456 KPLDRAVWIEFWYMRHKGAKHLRS 479  
 |||||||||||||||||||

## RESULT 10

UDP8\_RAT STANDARD; PRT; 530 AA.  
 ID UDP8\_RAT  
 AC 062789;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B8 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UGT2B-RH4).  
 GN UGT2B8.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H12G-;  
 RA Cohen H., Trus M., Benvenisty N., Reshef L.;  
 RT "A novel member of the UDPCT family is abundantly expressed in  
 RT H4IIEG3 hepatoma cells.";  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U27518; AAA86833.1; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPCT: 1.

DR PROSITE: PS00375; UDPCT: FALSE\_NEG.  
 KM Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 17  
 FT CHAIN 18 530 BY SIMILARITY.  
 FT TRANSMEM 496 516 UDP-GLUCURONOSYLTRANSFERASE 2B8.  
 FT CARBOHYD 316 316 POTENTIAL.  
 SQ SEQUENCE 530 AA; 60089 MW; 53251950C6CADE CRC64;

Query Match 4.4%; Score 23; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-15;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 453 KPLDRAVWIEFWYMRHKGAKHLR 475  
 Db 457 KPLDRAVWIEFWYMRHKGAKHLR 479  
 |||||||||||||||||||

## RESULT 11

UDP8\_HUMAN STANDARD; PRT; 530 AA.  
 ID UDP8\_HUMAN  
 AC P54855; P23765; Q9UK63;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B15 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UDPCTH-3) (HU04).  
 GN UGT2B15 OR UGT2B8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RC MEDLINE=95136867; PubMed=7835232;  
 RA Green M.D., Ocuru E.M., Tepfly T.R.;  
 RT "Stable expression of a human liver UDP-glucuronosyltransferase  
 RT (UGT2B15) with activity toward steroid and xenobiotic substrates.";  
 RL Drug Metab. Dispos. 22:79-805(1994).  
 RN [2]  
 RP SEQUENCE OF 8-530 FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RC MEDLINE=90343358; PubMed=2116769;  
 RA Coffman B.L., Tepfly T.R., Irishaid Y.M., Green M.D., Smith C.,  
 RA Jackson M.R., Wooster R., Burchell B.;  
 RT "Characterization and primary sequence of a human hepatic microsomal  
 RT estril UDPglucuronosyltransferase.";  
 RL Arch. Biochem. Biophys. 281:170-175(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT TYR-85.  
 RC MEDLINE=97439504; PubMed=9295060;  
 RA Levesque E., Beaulieu M., Green M.D., Tepfly T.R., Belanger A.,  
 RA Hum D.W.;  
 RT "Isolation and characterization of UGT2B15(Y85): a  
 RT UDP-glucuronosyltransferase encoded by a polymorphic gene.";  
 RL Pharmacogenetics 7:317-325(1997)  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD  
 CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES, INCLUDING SIMPLE  
 CC PHENOLIC COMPOUNDS, 7-HYDROXYLATED COMARINS, FLAVONOIDS,  
 CC ANTHRAQUINONES, AND CERTAIN DRUGS AND THEIR HYDROXYLATED  
 CC METABOLITES. IT ALSO CATALYZES THE GLUCURONIDATION OF ENDOGENOUS  
 CC ESTROGENS AND ANDROGENS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC CAUTION: REF.2 THOUGHT THAT THIS WAS A SEPARATE FORM (UGT2B8). THE  
 CC NAME UGT2B8 HAS NOW BEEN REUSED FOR A RAT ENZYME.





```

CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBIT.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L01083; AAA18020.1; -.
CC PIR: B47113; B47113.
CC InterPro: IPR002213; -.
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC Multigene family; Microsome.
CC -----
CC CHAIN 1 24 UDP-GLUCURONOSYLTRANSFERASE 2B13.
CC FT TRANSMEM 495 511 POTENTIAL.
CC FT CARBOHYD 69 69 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 317 317 N-LINKED (GLCNAC...) (POTENTIAL).
CC SO SEQUENCE 531 AA; 60552 MW; 961DA58AC4CB9932 CRC64;

Query Match 4.0%; Score 21; DB 1; Length 531;
Best Local Similarity 100.0%; Pred. No. 16e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 WIPONDILGHFKTKAFITHG 374
DB 358 WIPONDILGHFKTKAFITHG 378

RESULT 14
UDCL_RABBIT STANDARD; PRT; 502 AA.
AC P36514;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE (FRAGMENT).
GN UGT2C1 OR UGT2A2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
RX MEDLINE=93315511; PubMed=8325897;
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
RT "Cloning and characterization of rabbit liver UDP-
RT glucuronosyltransferase cDNAs. Developmental and inducible expression
RT of 4-hydroxydiphenyl UGT2B13."
RL J. Biol. Chem. 268:15260-15266(1993).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L01083; AAA18023.1; -.
CC PIR: B47113; B47113.
CC InterPro: IPR002213; -.
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane;
CC Multigene family; Microsome.
CC -----
CC CHAIN 1 1
CC FT TRANSMEM 466 481 POTENTIAL.
CC FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 288 288 N-LINKED (GLCNAC...) (POTENTIAL).
CC SO SEQUENCE 502 AA; 57449 MW; B5B65670BFAE1D35 CRC64;

Query Match 3.6%; Score 19; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 KPLDRAVFWIEFVRRKGA 471
DB 428 KPLDRAVFWIEFVRRKGA 446

RESULT 15
UDBR_HUMAN STANDARD; PRT; 529 AA.
AC O75310;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B11 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT).
GN UGT2B11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96340847; PubMed=9675083;
RA Beaulieu M., Levesque E., Hum D.W., Belanger A.;
RT "Isolation and characterization of a human orphan UDP-
RT glucuronosyltransferase, UGT2B11."
RL Biochem. Biophys. Res. Commun. 248:44-50(1998).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF016492; AAC27891.1; -.
CC MIM: 603064; -.
CC InterPro: IPR002213; -.
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC Multigene family; Microsome.
CC -----
CC CHAIN 1 21
CC FT SIGNAL 1 21 POTENTIAL.
CC FT TRANSMEM 493 513 UDP-GLUCURONOSYLTRANSFERASE 2B11.

```



FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 529 AA; 61038 MW; CEAA3C3C71CFC2AB4 CRC64;

Query Match 3.6%; Score 19; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDQPVKPLDRAVFWIEFVM 466  
DB 450 HDQPVKPLDRAVFWIEFVM 468

## RESULT 16

UDB3\_RAT STANDARD; PRT; 530 AA.  
ID UDB3\_RAT P08542; P16915;  
AC 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1990 (Rel. 15, Last annotation update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B3 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (TESTOSTERONE, DIHYDROTESTOSTERONE, AND BETA-ESTRADIOL SPECIFIC) (17-BETA-HYDROXYSTEROID SPECIFIC) (UDPCTR-3) (RUG38).  
GN UGT2B3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=87250645; PubMed=3110162;  
RA Mckenzie P.I.;  
RT "Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two enzymes which glucuronidate testosterone, dihydrotestosterone, and beta-estradiol.";  
RT J. Biol. Chem. 262:9744-9749(1987).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=87231096; PubMed=3108864;  
RA Harding D., Wilson S.M., Jackson M.R., Burchell B., Green M.D., Teply T.R.;  
RT "Nucleotide and deduced amino acid sequence of rat liver 17 beta-hydroxysteroid UDP-glucuronosyltransferase.";  
RT Nucleic Acids Res. 15:3936-3936(1987).  
CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS. 2B3 IS ACTIVE ON TESTOSTERONE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR BETA-D-GLUCORONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- INDUCTION: CONSTITUTIVELY EXPRESSED.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M1109; AAA1280.1; -  
CC EMBL; Y00156; CAA6351.1; -  
CC PIR; A28460; A28460.  
CC PIR; S07390; S07390.  
CC InterPro: IPR002213; -  
CC Pfam; PF00201; UDPCT; 1.  
CC PROSITE; PS00375; UDPCT; 1.  
CC Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT SIGNAL 1 23 BY SIMILARITY.

FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B3.  
FT TRANSMEM 494 510 POTENTIAL.  
FT CONFLICT 54 54 T -> S (IN CAA68351).  
FT CONFLICT 119 119 G -> E (IN REF. 2).  
FT CONFLICT 376 376 S -> G (IN REF. 2).  
FT CONFLICT 424 424 S -> T (IN REF. 2).  
FT CONFLICT 500 500 T -> S (IN REF. 2).  
SQ SEQUENCE 530 AA; 60524 MW; BB633D70DBE8A7E4 CRC64;

Query Match 3.4%; Score 18; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 458 AVFWIEFVRRHKGAKHLR 475  
DB 461 AVFWIEFVRRHKGAKHLR 478

## RESULT 17

UDBE\_RABIT STANDARD; PRT; 530 AA.  
ID UDBE\_RABIT P36513;  
AC 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B14 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (EGT12).  
GN UGT2B14.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_Taxid=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;  
RX MEDLINE=93315511; PubMed=8325897;  
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Teply T.R.;  
RT "Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.";  
RT J. Biol. Chem. 268:15260-15266(1993).  
RL -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR BETA-D-GLUCORONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L01082; AAA18021.1; -  
CC PIR; CA7113; CA7113.  
CC InterPro: IPR002213; -  
CC Pfam; PF00201; UDPCT; 1.  
CC PROSITE; PS00375; UDPCT; 1.  
CC Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT SIGNAL 1 24 BY SIMILARITY.  
FT CHAIN 25 530 UDP-GLUCURONOSYLTRANSFERASE 2B14.  
FT TRANSMEM 494 510 POTENTIAL.  
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 530 AA; 60664 MW; CEAA4BF25B53CB35 CRC64;

Query Match 3.4%; Score 18; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2, 1e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 YDMTPONDLLGHPRKAKF 369  
 DB 355 YDMTPONDLLGHPRKAKF 372

RESULT 18  
 UDB5\_MOUSE STANDARD; PRT; 530 AA.  
 ID UDB5\_MOUSE  
 AC P17717;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B5 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPGR) (M-1).  
 GN UGT2B5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6N; TISSUE=Liver;  
 RA MEDLINE=88029469; PubMed=3117546;  
 RX Kimura T., Owens I.S.;  
 RT "Mouse UDP glucuronosyltransferase. cDNA and complete amino acid  
 sequence and regulation.";  
 RL Eur. J. Biochem. 168:515-521(1987).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X06358; CAA29657.1; -;  
 DR PIR; S00163; S00163.  
 DR MGD; MGI:98900; Ugt2b5.  
 DR InterPro: IPR002213; -;  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 23  
 FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B5.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 530 AA; 60856 MW; 7BAFEE9EFA866B3 CRC64;

Query Match 3.2%; Score 17; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2, 2e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPLDRAVWFIEFVNRKH 469  
 DB 456 KPLDRAVWFIEFVNRKH 472

RESULT 19  
 UDB6\_RABIT STANDARD; PRT; 523 AA.  
 ID UDB6\_RABIT  
 AC O19103;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B16 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPGR) (FRAGMENT).  
 GN UGT2B16.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97166166; PubMed=9013565;  
 RA Li O., Lou X., Peyronneau M.-A., Straub P.O., Tukey R.H.;  
 RT "Expression and functional domains of rabbit liver UDP-  
 glucuronosyltransferase 2B16 and 2B13.";  
 RL J. Biol. Chem. 272:3272-3279(1997).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS. ACTS ON SMALL PHENOLIC AGENTS SUCH AS 2-  
 NAPHTHOL AND 4-METHYLBELLIFERONE AS WELL AS BULKY PHENOLIC  
 COMPOUNDS LIKE 2-HYDROXY- AND 4-HYDROXYBIPHENYL. IN CONTRAST TO  
 2B13 IT IS ACTIVE TOWARD 4-HYDROXYESTERONE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U72742; AB071494.1; -;  
 DR InterPro: IPR002213; -;  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT NON\_TER 1 1  
 FT SIGNAL 1 16  
 FT CHAIN 17 523 UDP-GLUCURONOSYLTRANSFERASE 2B16.  
 FT TRANSMEM 487 503 POTENTIAL.  
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 523 AA; 60077 MW; 22408BE768ED3DE CRC64;

Query Match 3.0%; Score 16; DB 1; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 2, 4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 460 FWIEFVNRKHGAKHHR 475  
 DB 456 FWIEFVNRKHGAKHHR 471

RESULT 20  
 UDB2\_RAT STANDARD; PRT; 530 AA.  
 ID UDB2\_RAT  
 AC P08541;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPGR) (3-HYDROXYANDROGEN SPECIFIC) (UDPGR-4) (RUG23).

GN UGT2B2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87033594; PubMed=2429951;  
 RA Mckenzie P.I.;  
 RT "Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression  
 of a form glucuronidating 3-hydroxyandrogens.";  
 RT J. Biol. Chem. 261:14112-14117(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91369480; PubMed=1909872;  
 RA Haque S.J., Peterson D.D., Nebert D.W., McKenzie P.I.;  
 RT "Isolation, sequence, and developmental expression of rat UGT2B2: the  
 gene encoding a constitutive UDP glucuronosyltransferase that  
 metabolizes etiocholanolone and androstereone.";  
 RT DNA Cell Biol. 10:515-524(1991).  
 RL [3]  
 RP SEQUENCE OF 30-530 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86120371; PubMed=3003696;  
 RA Jackson M.R., Burchell B.;  
 RT "The full length coding sequence of rat liver androstereone UDP-  
 glucuronyltransferase cDNA and comparison with other members of this  
 gene family.";  
 RT Nucleic Acids Res. 14:779-795(1986).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS. 2B2 ACTS ON VARIOUS ENDOGENOUS STEROIDS,  
 ESPECIALLY ETIOCHOLANOLONE AND ANDROSTERONE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 BETA-D-GLUCONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- INDUCTION: CONSTITUTIVELY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J02589; AAA2314.1; -  
 DR EMBL: M74459; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: X03478; CAA27198.1; -  
 DR PIR: A26064; A26064.  
 DR PIR: A23520; A23520.  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT; 1.  
 DR PROSITE: PS00375; UDPGT; 1.  
 KW transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT CHAIN 1 23  
 FT SIGNAL 1 23  
 FT TRANSMEM 24 530  
 FT CAROHYD 316 510  
 FT CONFLICT 159 159 D -> E (IN REF. 3).  
 FT CONFLICT 286 286 A -> S (IN REF. 3).  
 FT CONFLICT 351 351 N -> I (IN REF. 3).  
 FT CONFLICT 363 363 L -> I (IN REF. 3).  
 FT CONFLICT 363 363  
 FT SEQUENCE 530 AA; 60985 MW; F2FF3E23E2D75B2 CRC64;

Query Match 2.7%; Score 14; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPKTKAF 369  
 ||||||||||||  
 DB 359 PONDLLGHPKTKAF 372

## RESULT 21

UDP6\_RAT  
 ID UDP6\_RAT STANDARD; PRT; 530 AA.  
 AC P19468;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B6 PRECURSOR. MICROSOMAL (EC 2.4.1.17)  
 DE (UDPGT) (17-BETA-HYDROXYSTEROID SPECIFIC) (UDPGT-5).  
 GN UGT2B6.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90256795; PubMed=1692835;  
 RA Mckenzie P.I.;  
 RT "The cDNA sequence and expression of a variant 17 beta-hydroxysteroid  
 UDP-glucuronosyltransferase.";  
 RT J. Biol. Chem. 265:8699-8703(1990).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS. 2B6 IS ABOUT 30-FOLD LESS ACTIVE THAN 2B3  
 TOWARD TESTOSTERONE AND DIHYDROTESTOSTERONE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 BETA-D-GLUCONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- INDUCTION: CONSTITUTIVELY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M33746; AAA03216.1; -  
 DR EMBL: M33746; AAA03217.1; -  
 DR PIR: A36276; A36276.  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT; 1.  
 DR PROSITE: PS00375; UDPGT; 1.  
 KW transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT CHAIN 1 23  
 FT SIGNAL 1 23  
 FT TRANSMEM 24 530  
 FT TRANSMEM 494 510  
 FT SEQUENCE 530 AA; 60593 MW; F6B23E34569BDDEA CRC64;

Query Match 2.7%; Score 14; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPKTKAF 369  
 ||||||||||||  
 DB 359 PONDLLGHPKTKAF 372

## RESULT 22

UD16\_MOUSE  
 ID UD16\_MOUSE STANDARD; PRT; 531 AA.  
 AC 064435; 062580; P70692;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
 DE (UDPCT) (UGT1\*6) (UGT1-06) (UGT1.6) (UGT1A6) (UGT1A1) (PHENOL UDP-  
 GN GLUCURONOSYLTRANSFERASE).  
 GN UGT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/CBA; TISSUE=Liver;  
 RA Reuter S.F., Vasilion V., Puga A., Nebert D.W.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.  
 RC STRAIN=C57BL/6; TISSUE=Liver;  
 RX MEDLINE=94347791; PubMed=8068691;  
 RA Lamb J.G., Straub P., Tukey R.H.;  
 RT "Cloning and characterization of cDNAs encoding mouse Ugt1.6 and  
 RT rabbit UGT1.6: differential induction by  
 RT 2,3,7,8-tetrachlorodibenzo-p-dioxin";  
 RL Biochemistry 33:10513-10520(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=95408245; PubMed=7677729;  
 RA Koike O., Hasada K., Yasui Y., Sakai Y., Sato H., Watanabe T.;  
 RT "Isolation of cDNAs for mouse phenol and bilirubin UDP-  
 RT glucuronosyltransferases and mapping of the mouse gene for phenol  
 RT UDP-glucuronosyltransferase (Ugt1a) to chromosome 1 by restriction  
 RT fragment length variations";  
 RL Biochem. Genet. 33:111-122(1995).  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. CONJUGATES SMALL PLANAR PHENOLIC MOLECULES  
 CC SUCH AS 4-NITROPHENOL, 1-NAPHTHOL, AND 4-METHYLBELLIFERONE. THE  
 CC BULKY PHENOL 4-HYDROXYBIPHENYL, ANDROGENS AND ESTROGENS ARE NOT  
 CC SUBSTRATES. 2-HYDROXYBIPHENYL IS AN EXCELLENT SUBSTRATE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- INUNCTION: BY DIOXIN.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: U16818; AAA65979.1; -  
 DR EMBL: U09930; AAA51871.1; -  
 DR EMBL: D87867; BAA13483.1; -  
 DR MGD: MGI:98898; Ugt1a1.  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT; 1.  
 DR PROSITE: PS00375; UDPGT; 1.  
 KW Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 531  
 FT TRANSMEM 489 505  
 FT CARBOHYD 293 293  
 FT CARBOHYD 431 431  
 FT CONFLICT 43 43  
 FT CONFLICT 69 69  
 FT CONFLICT 104 104  
 S -> L (IN REF. 3).  
 FT CONFLICT 104 104

FT CONFLICT 225 225 L -> P (IN REF. 3).  
 FT CONFLICT 466 466 H -> K (IN REF. 2).  
 SO SEQUENCE 531 AA; 60438 MW; AE7CASF5C818DC12 CRC64;

Query Match 2.1%; Score 11; DB 1; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 0.0035;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLDGPKT 366  
 DB 354 PONDLDGPKT 364

RESULT 23  
 ID UDP12 MOUSE STANDARD; PRT; 533 AA.  
 AC P70691;  
 DE 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
 DE (UDPCT) (UGT1\*0) (UGT1-02) (UGT1.2) (UGT1A2) (BILIRUBIN SPECIFIC).  
 GN UGT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=95408245; PubMed=7677729;  
 RA Koike O., Hasada K., Yasui Y., Sakai Y., Sato H., Watanabe T.;  
 RT "Isolation of cDNAs for mouse phenol and bilirubin UDP-  
 RT glucuronosyltransferases and mapping of the mouse gene for phenol  
 RT UDP-glucuronosyltransferase (Ugt1a) to chromosome 1 by restriction  
 RT fragment length variations";  
 RL Biochem. Genet. 33:111-122(1995).  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR =  
 CC UDP + ACCEPTOR BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFT. (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: D87866; BAA13482.1; -  
 DR MGD: MGI:98898; Ugt1a1.  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT; 1.  
 DR PROSITE: PS00375; UDPGT; 1.  
 KW Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 27  
 FT CHAIN 28 533  
 FT TRANSMEM 491 511  
 FT CARBOHYD 141 141  
 FT CARBOHYD 295 295  
 FT CARBOHYD 433 433  
 FT CONFLICT 533 AA; 60285 MW; FB4584395255050A CRC64;

Query Match 2.1%; Score 11; DB 1; Length 533;  
 Best Local Similarity 100.0%; Pred. No. 0.0035;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 366  
 DB 356 PONDGLGHPK 366

## RESULT 24

UD16\_RAT STANDARD; PRT: 529 AA.

AC P08430;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOFTAL (EC 2.4.1.17)  
 DE (UDPGT) (UGT1\*6) (UGT1-06) (UGT1A6) (A1) (P-NITROPHENOL SPECIFIC).  
 GN UGT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MISTAR;  
 RX MEDLINE=87057193; PubMed=3096993;  
 RA Iyanagi T., Hanui M., Sogawa K., Fujii-Kuriyama Y., Watanabe S.,  
 RA Shively J.E., Anan K.F.;  
 RT "Cloning and characterization of cDNA encoding 3-methylcholanthrene  
 RT inducible rat mRNA for UDP-glucuronosyltransferase.";  
 RL J. Biol. Chem. 261:15607-15614(1986)

CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFTAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: J02612; AAA42311.1; -;  
 DR PIR: A24600; A24600.  
 DR InterPro: IPR002213; -;  
 DR Pfam: PF00201; UDPGT. 1.  
 DR PROSITE: PS00375; UDPGT. 1.  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KM Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 25  
 FT CHAIN 26 529 UDP-GLUCURONOSYLTRANSFERASE 1-6.  
 FT TRANSMEM 487 503 POTENTIAL.  
 FT CARBOHYD 281 281 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 291 291 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 429 429 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA; 60132 MW; 144ACDA7EDDE04B CRC64;

DB 352 PONDGLGHPK 361

## RESULT 25

UD18\_RAT STANDARD; PRT: 530 AA.

AC Q64634;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-8 PRECURSOR, MICROSOFTAL (EC 2.4.1.17)  
 DE (UDPGT) (UGT1\*8) (UGT1-08) (UGT1A8) (A3).  
 GN UGT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MISTAR;  
 RX MEDLINE=95332265; PubMed=7608130;  
 RA Eml Y., Ikushiro S.I., Iyanagi T.;  
 RT "Drug-responsive and tissue-specific alternative expression of 1  
 RT multiple first exons in rat UDP-glucuronosyltransferase family 1  
 RT (UGT1) gene complex.";  
 RL J. Biochem. 117:392-399(1995).  
 RN [2]  
 RP SEQUENCE OF 286-530 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90274676; PubMed=2112380;  
 RA Sato H., Koizumi O., Tanabe K., Kashiwamata S.;  
 RT "Isolation and sequencing of rat liver bilirubin UDP-  
 RT glucuronosyltransferase cDNA: possible alternate splicing of a common  
 RT primary transcript.";  
 RL Biochem. Biophys. Res. Commun. 169:260-264(1990).

CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFTAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: D38063; BA07259.1; -;  
 DR EMBL: M34007; AAA42312.1; ALT-TERM.  
 DR InterPro: IPR002213; -;  
 DR Pfam: PF00201; UDPGT. 1.  
 DR PROSITE: PS00375; UDPGT. 1.  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KM Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 25  
 FT CHAIN 26 530 UDP-GLUCURONOSYLTRANSFERASE 1-8.  
 FT TRANSMEM 488 504 POTENTIAL.  
 FT CARBOHYD 71 71 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 292 292 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 430 430 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 530 AA; 60060 MW; 507098AEB1D4AC5C CRC64;

Query Match 1.9%; Score 10; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 365

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 PONDGLGHPK 365  
 |||||  
 Db 353 PONDGLGHPK 362

RESULT 26  
 ID U013\_RAT STANDARD: PRT: 531 AA.  
 AC Q64637;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UGT1\*3) (UGT1-03) (UGT1A3) (B5).  
 GN UGT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-286 FROM N.A.  
 RC STRAIN-WISTAR;  
 RX MEDLINE=95332265; PubMed=7608130;  
 RA Eml Y., Ikushiro S.I., Iyanagi T.;  
 RT "Drug-responsive and tissue-specific alternative expression of  
 multiple first exons in rat UDP-glucuronosyltransferase family 1  
 (UGT1) gene complex.";  
 RT J. Biochem. 117:392-399(1995).  
 RL [2]  
 RN SEQUENCE OF 287-531 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90274676; PubMed=2112380;  
 RA Sato H., Koizumi O., Tanabe K., Kashiwamata S.;  
 RT "Isolation and sequencing of rat liver bilirubin UDP-  
 glucuronosyltransferase cDNA: possible alternate splicing of a common  
 primary transcript.";  
 RT Biochem. Biophys. Res. Commun. 169:260-264(1990).  
 RL [1]  
 RN FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC -1- BETA-D-GLUCORONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D38067; BAA07262.1; -  
 CC EMBL: M34007; AAA42312.1; ALT\_TERM.  
 DR InterPro: IPR002213;  
 DR Pfam: PF00201; UDPCT; 1.  
 DR PROSITE: PS00375; UDPCT; 1.  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 25  
 FT CHAIN 26 531  
 FT TRANSMEM 489 505  
 FT CARBOHYD 116 139  
 FT CARBOHYD 293 293  
 FT CARBOHYD 431 431  
 FT CARBOHYD 531 AA; 60140 MW; EC80994C6A2C7CE6; CRG64;  
 SQ SEQUENCE

Query Match 1.9%; Score 10; DB 1; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 365  
 |||||  
 Db 354 PONDGLGHPK 363

RESULT 27  
 ID U015\_RAT STANDARD: PRT: 531 AA.  
 AC Q64638;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-5 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UGT1\*5) (UGT1-05) (UGT1A5) (B5).  
 GN UGT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-286 FROM N.A.  
 RC STRAIN-WISTAR;  
 RX MEDLINE=95332265; PubMed=7608130;  
 RA Eml Y., Ikushiro S.I., Iyanagi T.;  
 RT "Drug-responsive and tissue-specific alternative expression of  
 multiple first exons in rat UDP-glucuronosyltransferase family 1  
 (UGT1) gene complex.";  
 RT J. Biochem. 117:392-399(1995).  
 RL [2]  
 RN SEQUENCE OF 287-531 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90274676; PubMed=2112380;  
 RA Sato H., Koizumi O., Tanabe K., Kashiwamata S.;  
 RT "Isolation and sequencing of rat liver bilirubin UDP-  
 glucuronosyltransferase cDNA: possible alternate splicing of a common  
 primary transcript.";  
 RT Biochem. Biophys. Res. Commun. 169:260-264(1990).  
 RL [1]  
 RN FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC -1- BETA-D-GLUCORONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D38069; BAA07263.1; -  
 CC EMBL: M34007; AAA42312.1; ALT\_TERM.  
 DR InterPro: IPR002213;  
 DR Pfam: PF00201; UDPCT; 1.  
 DR PROSITE: PS00375; UDPCT; 1.  
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 25  
 FT CHAIN 26 531  
 FT TRANSMEM 489 505  
 FT CARBOHYD 116 116  
 FT CARBOHYD 116 116  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 531 AA: 59993 MW: 04148C1BACAC80 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 531;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365  
Db 354 PONDLLGHPK 363

RESULT 28  
UD12\_RAT  
ID UD12\_RAT STANDARD; PRT; 531 AA.  
AC 064633;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (UGT1\*7) (UGT1-07) (UGT1A7) (A2).  
GN UGT1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE OF 1-286 FROM N.A.  
RC STRAIN=WISTAR;  
RC MEDLINE=95332265; PubMed=7608130;  
RA Emi Y., Ikushiro S.I., Iyanagi T.;  
RT "Drug-responsive and tissue-specific alternative expression of  
RT multiple first exons in rat UDP-glucuronosyltransferase family 1  
RT (UGT1) gene complex.";  
RT J. Biochem. 117:392-399(1995).  
RN [2]  
RP SEQUENCE OF 287-531 FROM N.A.  
RC TISSUE=Liver;  
RC MEDLINE=90274676; PubMed=2112380;  
RA Sato H., Koizumi O., Tanabe K., Kashimawata S.;  
RT "Isolation and sequencing of rat liver bilirubin UDP-  
RT glucuronosyltransferase cDNA: possible alternate splicing of a common  
RT primary transcript.";  
RL Biochem. Biophys. Res. Commun. 169:260-264(1990).  
RL -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: D38062; BAA07258.1; -  
CC EMBL: M34007; AAA42312.1; ALT\_TERM.  
CC InterPro: IPR002213; -  
CC Pfam: PF00201; UDPGT; 1.  
CC PROSITE: PS00375; UDPGT; 1.  
CC Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW

KW Multigene family; Microsome; Alternative splicing.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 531 UDP-GLUCURONOSYLTRANSFERASE 1-7.  
FT TRANSMEM 487 503 POTENTIAL.  
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 531 AA: 59627 MW: BC791DEC724CA621 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 531;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365  
Db 354 PONDLLGHPK 363

RESULT 29  
UD12\_RAT  
ID UD12\_RAT STANDARD; PRT; 533 AA.  
AC P20720; 064636;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (UGT1\*0) (UGT1-02) (UGT1A2) (BILIRUBIN SPECIFIC)  
DE (B2).  
GN UGT1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RC MEDLINE=90274676; PubMed=2112380;  
RA Sato H., Koizumi O., Tanabe K., Kashimawata S.;  
RT "Isolation and sequencing of rat liver bilirubin UDP-  
RT glucuronosyltransferase cDNA: possible alternate splicing of a common  
RT primary transcript.";  
RL Biochem. Biophys. Res. Commun. 169:260-264(1990).  
RN [2]  
RP SEQUENCE OF 1-288 FROM N.A.  
RC STRAIN=WISTAR;  
RC MEDLINE=95332265; PubMed=7608130;  
RA Emi Y., Ikushiro S.I., Iyanagi T.;  
RT "Drug-responsive and tissue-specific alternative expression of  
RT multiple first exons in rat UDP-glucuronosyltransferase family 1  
RT (UGT1) gene complex.";  
RT J. Biochem. 117:392-399(1995).  
RN [2]  
RP SEQUENCE OF 289-533 FROM N.A.  
RC TISSUE=Liver;  
RC MEDLINE=90274676; PubMed=2112380;  
RA Sato H., Koizumi O., Tanabe K., Kashimawata S.;  
RT "Isolation and sequencing of rat liver bilirubin UDP-  
RT glucuronosyltransferase cDNA: possible alternate splicing of a common  
RT primary transcript.";  
RL Biochem. Biophys. Res. Commun. 169:260-264(1990).  
RL -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: M34007; AAA42312.1; -  
CC EMBL: D38066; BAA07261.1; -



```
DR PIR: A35343; A35343.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1 27
FT CHAIN 28 533
FT TRANSFER 491 507
FT CARBOHYD 133 133
FT CARBOHYD 141 141
FT CARBOHYD 295 295
FT CARBOHYD 433 433
FT CONFLICT 2 3
FT CONFLICT 177 178
SQ SEQUENCE 533 AA; 60045 MW; 5A9E974EF7EBAF5B CRC64;

Query Match
Best Local Similarity 1.9%; Score 10; DB 1; Length 533;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 365
DB 356 PONDGLGHPK 365

RESULT 30
UD11_RAT
ID UD11_RAT STANDARD; PRT; 535 AA.
AC 064550; 064635;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1*1) (UGT1-01) (UGT1A1) (BL).
GN UGT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95327065; PubMed=7603447;
RA Coffman B.L., Green M.D., King C.O., Tephly T.R.;
RT "Cloning and stable expression of a cDNA encoding a rat liver UDP-
RT glucuronosyltransferase (UDP-glucuronosyltransferase 1.1) that
RT catalyzes the glucuronidation of opioids and bilirubin."
RL Mol. Pharmacol. 47:1101-1105(1995).
RN [2]
RP SEQUENCE OF 1-290 FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95332265; PubMed=7608130;
RA Eml Y., Iwashiro S.T., Iyanagi T.;
RT "Drug-responsive and tissue-specific alternative expression of
RT multiple first exons in rat UDP-glucuronosyltransferase family 1
RT (UGT1) gene complex."
RL J. Biochem. 117:392-399(1995).
RN [3]
RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
RN SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
RN ENDOGENOUS COMPOUNDS. GLUCURONATES OPIOIDS AND BILIRUBIN.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```

```
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U20551; AAC52219.1; -.
DR EMBL: D38065; BAA07260.1; -.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 535
FT TRANSFER 493 509
FT CARBOHYD 89 89
FT CARBOHYD 297 297
FT CARBOHYD 435 435
FT CONFLICT 253 253
SQ SEQUENCE 535 AA; 59662 MW; 26B642FCA7DD4082 CRC64;

Query Match
Best Local Similarity 1.9%; Score 10; DB 1; Length 535;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 365
DB 358 PONDGLGHPK 367

RESULT 31
UD17_MOUSE
ID UD17_MOUSE STANDARD; PRT; 520 AA.
AC 062452;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1*7) (UGT1-07) (UGT1A7) (UGT1A4) (FRAGMENT).
GN UGT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=93219265; PubMed=8464825;
RA Kong A.N., Ma M., Tao D., Yang L.;
RT "Molecular cloning of two cDNAs encoding the mouse bilirubin/phenol
RT family of UDP-glucuronosyltransferases (mUGTbr/P).";
RL Pharm. Res. 10:461-465(1993).
RN [2]
RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
RN SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
RN ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L27122; AAA40524.1; ALT_INT.
```

```

DR MGD: MGI:98898: Ugt1a1.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KM Multigene family; Microsome; Alternative splicing.
FT SIGNAL: 1
FT CHAIN: 1
FT TRANSMEM: 16 520 UDP-GLUCURONOSYLTRANSFERASE 1-7.
FT CARBOHYD: 61 494 POTENTIAL.
FT CARBOHYD: 282 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD: 420 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD: 420 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 520 AA; 59193 MW; 2048D5C5CDAC895 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
| | | | | | | | | |
DB 288 GIVFSLGS 296

RESULT 32
ID ID12_HUMAN STANDARD; PRT; 530 AA.
AC P36509;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1-1B) (UGT1-02) (UGT1A2) (UGT1B)
DE (HLUGP4).
GN UGT1 OR GNT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91378895; PubMed=1910331;
RA Wooster R., Sutherland L., Ebner T., Clarke D., E Silva O.,
RA Burchell B.;
RT "Cloning and stable expression of a new member of the human liver
RT phenol/bilirubin: UDP-glucuronosyltransferase cDNA family.";
RL Biochem. J. 278:465-469(1991).
RN [2]
RP SEQUENCE OF 286-530 FROM N.A.
RX MEDLINE=92147680; PubMed=1339448;
RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,
RA Owens I.S.;
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and
RT other UDP-glucuronosyltransferase isozymes with identical carboxyl
RT terminl.";
RL J. Biol. Chem. 267:3257-3261(1992).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S55985; AAB19791.2; -.
DR PIR: S17512; S17512.
DR MIM: 191740; -.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KM Multigene family; Microsome; Alternative splicing.
FT SIGNAL: 1
FT CHAIN: 26 530 UDP-GLUCURONOSYLTRANSFERASE 1-2.
FT TRANSMEM: 488 504 POTENTIAL.
FT CARBOHYD: 292 524 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD: 344 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT: 301 301 V -> G (IN REF. 1).
FT CONFLICT: 340 340 S -> C (IN REF. 1).
FT CONFLICT: 364 364 R -> S (IN REF. 1).
FT CONFLICT: 410 364 L -> M (IN REF. 1).
FT CONFLICT: 419 419 D -> E (IN REF. 1).
FT CONFLICT: 469 469 P -> T (IN REF. 1).
FT CONFLICT: 495 495 V -> A (IN REF. 1).
FT CONFLICT: 504 504 F -> C (IN REF. 1).
SQ SEQUENCE 530 AA; 60018 MW; 9075B002010B67CE CRC64;

Query Match 1.7%; Score 9; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
| | | | | | | | | |
DB 298 GIVFSLGS 306

RESULT 33
ID ID16_HUMAN STANDARD; PRT; 531 AA.
AC P19224;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1-1F) (UGT1*6) (UGT1A6) (UGT1F) (PHENOL
DE SPECIFIC).
GN UGT1 OR GNT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147680; PubMed=1339448;
RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,
RA Owens I.S.;
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and
RT other UDP-glucuronosyltransferase isozymes with identical carboxyl
RT terminl.";
RL J. Biol. Chem. 267:3257-3261(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89042187; PubMed=3141926;
RA Harding D., Fournel-gigleux S., Jackson M.R., Burchell B.;
RT "Cloning and substrate specificity of a human phenol UDP-
RT glucuronosyltransferase expressed in COS-7 cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:8381-8385(1988).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.

```

```

CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M84130; AAC41717.1; -
CC EMBL: M84124; AAA61247.1; ALT SEQ.
CC EMBL: M84122; AAA61247.1; JOINED.
CC EMBL: M84123; AAA61247.1; JOINED.
CC EMBL: J04093; AAA61251.1; -
CC PIR: A31340; A31340.
CC MIM: 191740; -
CC InterPro: IPR002213; -
CC Pfam: PF00201; UDPGT: 1.
CC PROSITE: PS00375; UDPGT: 1.
CC DR TRANSFERASE: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC KM Multigene family; Microsome; Alternative splicing.
CC FT SIGNAL 1 ?
CC FT CHAIN 1 ?
CC FT TRANSFERASE 489 505 UDP-GLUCURONOSYLTRANSFERASE 1-6.
CC FT CARBOHYD 293 293 N-LINKED (GLCNC. . .) (POTENTIAL).
CC FT CARBOHYD 345 345 N-LINKED (GLCNC. . .) (POTENTIAL).
CC FT CONFLICT 70 70 Y -> S (IN REF. 2).
CC FT CONFLICT 231 231 K -> E (IN REF. 2).
CC FT CONFLICT 247 248 SE -> YOK (IN REF. 2).
CC FT CONFLICT 327 327 N -> I (IN REF. 2).
CC FT CONFLICT 509 509 P -> A (IN REF. 2).
CC FT CONFLICT 513 513 P -> R (IN REF. 2).
CC SEQUENCE 531 AA; 60590 MW; AA62AD6DFPAC823C CRC64;
SQ

```

Query Match  
Best Local Similarity 1.7%; Score 9; DB 1; Length 531;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 301 GIVFSLGS 309
DB 299 GIVFSLGS 307

```

RESULT 34  
UD16\_RABIT  
ID UD16\_RABIT STANDARD: PRT: 531 AA.  
AC 028611;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPGT) (UGT1\*6) (UGT1-06) (UGT1A6).  
GN UGT1.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.  
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;  
RX MEDLINE=84347791; PubMed=808691;  
RA Lamb J.G., Straub P., Tukey R.H.;  
RT Cloning and characterization of cDNAs encoding mouse Ugt1.6 and  
RT rabbit Ugt1.6: differential induction by  
RT 2,3,7,8-tetrachlorodibenzo-p-dioxin.  
RL Biochemistry 33:10513-10520(1994).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

```

CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS. CONJUGATES SMALL PLANAR PHENOLIC MOLECULES
CC SUCH AS 4-NITROPHENOL, 1-NAPHTHOL, AND 4-METHYLBELLIFERONE. THE
CC BULKY PHENOL 4-HYDROXYBIPHENYL, ANDROGENS AND ESTROGENS ARE NOT
CC SUBSTRATES. 2-HYDROXYBIPHENYL IS AN EXCELLENT SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES (BY SIMILARITY).
CC -1- INDUCTION: BY DIOXIN.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U09030; AAA51867.1; -
CC InterPro: IPR002213; -
CC Pfam: PF00201; UDPGT: 1.
CC PROSITE: PS00375; UDPGT: 1.
CC DR TRANSFERASE: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC KM Multigene family; Microsome; Alternative splicing.
CC FT SIGNAL 1 26
CC FT CHAIN 27 531 UDP-GLUCURONOSYLTRANSFERASE 1-6.
CC FT TRANSFERASE 489 505 POTENTIAL.
CC FT CARBOHYD 294 294 N-LINKED (GLCNC. . .) (POTENTIAL).
CC SEQUENCE 531 AA; 60098 MW; 872D317852F0928F CRC64;
SQ

```

Query Match  
Best Local Similarity 1.7%; Score 9; DB 1; Length 531;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 301 GIVFSLGS 309
DB 300 GIVFSLGS 308

```

RESULT 35  
UD14\_RABIT  
ID UD14\_RABIT STANDARD: PRT: 532 AA.  
AC 028612;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPGT) (UGT1\*4) (UGT1-04) (UGT1A4).  
GN UGT1.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;  
RA Philipp T., Durazac W., Trautwein C., Alex B., Johnson E.F.,  
RA Straub J.G., Straub P., Tukey R.H., Manns M.;  
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES (BY SIMILARITY).





FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 534 AA: 60338 MW: 9C5833652A4D9B3D CRC64;

Query Match 1.7%; Score 9; DB 1; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309  
Db 302 GIVFSLGS 310

RESULT 38  
UD14\_HUMAN STANDARD; PRT: 534 AA.  
ID UD14\_HUMAN  
AC P22310;  
DT 01-AUG-1991 (Rel. 19, created)  
DT 01-AUG-1991 (Rel. 19, last sequence update)  
DT 01-OCT-2000 (Rel. 40, last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
DE (UDPGLT) (UGT-1D) (UGT1-4) (UGT1A4) (UGT1D)  
DE (BILIRUBIN SPECIFIC ISOZYME 2) (HUG-BR2).  
GN UGT1 OR GNT1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=91093210; PubMed=1898728;  
RA Rittler J.K., Crawford J.M., Owens I.S.;  
RT "Cloning of two human liver bilirubin UDP-glucuronosyltransferase  
RL J. Biol. Chem. 266:1043-1047(1991).  
[2]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RX MEDLINE=92147680; PubMed=1339448;  
RA Rittler J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,  
OWENS I.S.;  
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and  
RL other UDP-glucuronosyltransferase isozymes with identical carboxyl  
termini." J. Biol. Chem. 267:3257-3261(1992).  
[3]  
RP VARIANT CN-I PHE-376.  
RX MEDLINE=92339803; PubMed=1634050;  
RA Bosma P.J., Chowdhury J.R., Huang T.-J., Lahiri P., Elfeink R.P.J.O.,  
van Es H.H.G., Lederstein M., Whittington P.F., Jansen P.L.,  
Chowdhury N.R.;  
RT "Mechanisms of inherited deficiencies of multiple UDP-  
RL glucuronosyltransferase isoforms in two patients with Crigler-Najjar  
syndrome, type I." J. Biol. Chem. 268:2859-2863(1992).  
[4]  
RP VARIANTS CN-II PRO-132 AND ASP-487.  
RX MEDLINE=94107323; PubMed=8280139;  
RA Aono S., Yamada Y., Kellno H., Hanada N., Nakagawa T., Sasaoka Y.,  
Yazawa T., Sato H., Kojima O.;  
RT "Identification of defect in the genes for bilirubin UDP-glucuronosyl-  
RL transferase in a patient with Crigler-Najjar syndrome type II." J.  
Biochem. Biophys. Res. Commun. 197:1239-1244(1993).  
[5]  
RP VARIANT CN-II ARG-332.  
RX MEDLINE=94102756; PubMed=8276413;  
RA Moghribi N., Clarke D.J., Boxer M., Burchell B.;  
RT "Identification of an A-to-G missense mutation in exon 2 of the UGT1  
RL gene complex that causes Crigler-Najjar syndrome type 2." J.  
Genomics 18:171-173(1993).  
CC -1- FUNCTION: UDPGLT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS, GLUCURONIDATES BILIRUBIN IX-ALPHA TO FORM  
CC BOTH THE IX-ALPHA-C8 AND IX-ALPHA-C12 MONOCONJUGATES AND  
CC DISCONJUGATE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER. NOT EXPRESSED IN SKIN OR  
CC KIDNEY.  
CC -1- INDUCTION: BY PHENOBARBITAL.  
CC -1- DISEASE: THE GILBERT'S SYNDROME IS SHOWN TO OCCUR AS A CONSEQUENCE  
CC OF REDUCED BILIRUBIN TRANSFERASE ACTIVITY. THE DISORDER, IS MOST  
CC OFTEN DETECTED IN YOUNG ADULTS WITH VAGUE NONSPECIFIC COMPLAINTS.  
CC A MORE SEVERE INHERITABLE DEFICIENCY IN BILIRUBIN ACTIVITY EXIST  
CC IN CRIGLER-NAJJAR (CN): PATIENTS WITH TYPE I (RECESSIVE TRAIT)  
CC HAVE SEVERE HYPERBILIRUBINEMIA AND USUALLY DIE OF KERNICTERUS  
CC (BILIRUBIN ACCUMULATION IN THE BASAL GANGLIA AND BRAINSTEM NUCLEI)  
CC WITHIN THE FIRST YEAR OF LIFE. PATIENTS WITH TYPE II (DOMINANT  
CC TRAIT) HAVE LESS SEVERE HYPERBILIRUBINEMIA AND USUALLY SURVIVE  
CC INTO ADULTHOOD WITHOUT NEUROLOGIC DAMAGE. PHENOBARBITAL, WHICH  
CC INDUCES THE PARTIALLY DEFICIENT GLUCURONYL TRANSFERASE, CAN  
CC DIMINISH THE JAUNDICE.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
-----  
CC EMBL: M84128; AAA61249.1; -;  
DR EMBL: M84124; AAA61247.1; ALT. SEQ.  
DR EMBL: M84123; AAA61247.1; JOINED.  
DR EMBL: M57951; AAA63196.1; -;  
DR PIR: B39092; B39092.  
DR MIM: 191740; -;  
DR MIM: 143500; -;  
DR MIM: 218800; -;  
DR InterPro: IPR002213; -;  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Alternative splicing; Disease mutation.  
FT SIGNAL 1 28  
FT CHAIN 29 534  
FT TRANSMEM 492 508  
FT CARBOHYD 119 119  
FT CARBOHYD 142 142  
FT CARBOHYD 296 296  
FT CARBOHYD 348 348  
FT VARIANT 132 132  
FT VARIANT 332 332  
FT VARIANT 376 376  
FT VARIANT 487 487  
FT SEQUENCE 534 AA: 60025 MW: AB745D46F538BE CRC64;  
Query Match 1.7%; Score 9; DB 1; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 301 GIVFSLGS 309  
Db 302 GIVFSLGS 310

RESULT 39  
ID15\_HUMAN STANDARD; PRT; 534 AA.  
AC P35504;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-5 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (UGT1-1E) (UGT1-5) (UGT1A5) (UGT1E).  
GN UGT1 OR GNT1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92147680; PubMed=1339448;  
RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,  
Owens I.S.;  
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and  
RT other UDP-glucuronosyltransferase isozymes with identical catalytic  
RT termini.";  
RL J. Biol. Chem. 267:3257-3261(1992).  
CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
-----  
DR EMBL: M84129; AAA61250.1; -  
DR EMBL: M84124; AAA61247.1; ALT\_SEQ.  
DR EMBL: M84122; AAA61247.1; JOINED.  
DR EMBL: M84123; AAA61247.1; JOINED.  
DR MIM: 191740;  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPCT.1.  
DR PROSITE: PS00375; UDPCT.1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Alternative splicing.  
FT SIGNAL 1  
FT CHAIN 1  
FT TRANSMEM 29 534 UDP-GLUCURONOSYLTRANSFERASE 1-5.  
FT CARBOHYD 492 508 POTENTIAL.  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 534 AA; 60071 MW; 05989F2A18EFAA4 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309  
Db 302 GIVFSLGS 310

RESULT 40

UDP1\_MOUSE  
ID UDP1\_MOUSE STANDARD; PRT; 535 AA.  
AC O63886;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (UGT1\*1) (UGT1-01) (UGT1A1) (UGTBR1).  
GN UGT1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93219265; PubMed=8464825;  
RA Kong A.N., Ma M., Tao D., Yang L.;  
RT "Molecular cloning of two cDNAs encoding the mouse bilirubin/phenol  
RT family of UDP-glucuronosyltransferases (mUGTbr/p).";  
RL Pharm. Res. 10:461-465(1993).  
CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- SIMILARITY: BY DIOXIN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
-----  
DR EMBL: S64760; AA26033.2; -  
DR MGD: MGI:98896; Ugt1a1.  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPCT.1.  
DR PROSITE: PS00375; UDPCT.1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Alternative splicing.  
FT SIGNAL 1  
FT CHAIN 1  
FT TRANSMEM 30 535 UDP-GLUCURONOSYLTRANSFERASE 1-1.  
FT CARBOHYD 493 509 POTENTIAL.  
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 535 AA; 60123 MW; B5AE3C209979BBB8 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 535;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309  
Db 303 GIVFSLGS 311

RESULT 41  
ID FER\_BUMFT STANDARD; PRT; 98 AA.  
AC P13106;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE FERREDOXIN.



```

OS Bumilleropsis filiformis.
OC Eukaryota; Stramenopiles; Xanthophyceae; Bumilleropsis.
OX NCBI_TaxID=2835;
RN [1]
RP SEQUENCE.
RX MEDLINE=84087800; PubMed=6418731;
RA Inoue K., Hase T., Boeger P., Matsubara H.;
RT "Amino acid sequence of a ferredoxin from Bumilleropsis filiformis,
a yellow-green alga: relationship with red algae,
Protochlorocephyceae, and filamentous blue-green algae.";
RT Prochlorocephyceae, and filamentous blue-green algae.";
RT J. Biochem. 94:1451-1455(1983).
CC -1- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
CC -1- COFACTOR: BINDS A 2FE-2S CLUSTER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
DR HSP: P00246; FEH2.
DR HSP: P00246; FEH2.
DR InterPro: IPR000564; -.
DR Pfam: PF00111; Fer2; 1.
DR PRINTS: PR00159; 2FE2SFERDOXIN.
DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
KM Electron transport; Iron-sulfur; Chloroplast.
FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 46 46 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 49 49 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT VARIANT 1 1 E -> A.
SQ SEQUENCE 98 AA; 10620 MW; E49CCDAC01DD75E CRC64;

Query Match 1.5%; Score 8; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 493 GFLTCVA 500
DB 74 GFLTCVA 81

RESULT 42
HEM1_CLOJO
ID HEM1_CLOJO STANDARD; PRT; 515 AA.
AC 059292;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.1-) (GLUTR).
GN HEMA.
OS Clostridium josui.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1499;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PERM P-9684;
RX MEDLINE=95394829; PubMed=7665501;
RA Fujino E., Fujino T., Karita S., Sakka K., Ohmiya K.;
RT "Cloning and sequencing of some genes responsible for porphyrin
biosynthesis from the anaerobic bacterium Clostridium josui.";
RT J. Bacteriol. 177:5169-5175(1995).
CC -1- FUNCTION: IT MAY BE INVOLVED IN THE SYNTHESIS OF 5-AMINOLEVULINIC
ACID (ALA) FROM GLUTAMATE AND IN THAT OF SYROHEME FROM PRECORRIN-
2.
CC -1- CATALYTIC ACTIVITY: GLUTAMYL-TRNA(GLU) + NADPH = GLUTAMATE-1-
SEMIALDEHYDE + NADP(+) + TRNA(GLU).
CC -1- PATHWAY: SYROHEME BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMYL-TRNA REDUCTASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D28503; BAA05860.1; -.
DR InterPro: IPR000343; -.
DR Pfam: PF00745; GLUTR; 1.
DR PROSITE: PS00747; GLUTR; 1.
KW Porphyrin biosynthesis; Oxidoreductase; NADP.
SQ SEQUENCE 515 AA; 58368 MW; A9769824AA30DC4C CRC64;

Query Match 1.5%; Score 8; DB 1; Length 515;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 EIFVDL 95
DB 285 EIFVDL 292

RESULT 43
CGT_HUMAN
ID CGT_HUMAN STANDARD; PRT; 541 AA.
AC 016880; 000196;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 2-HYDROXYACETYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR
DE (EC 2.4.1.45) (UDP-GALACTOSE-CERAMIDE GALACTOSYLTRANSFERASE) (CERAMIDE
DE UDP-GALACTOSYLTRANSFERASE) (CEREBROSIDE SYNTHASE).
GN UDP8 OR CGT OR UGT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299661; PubMed=8661025;
RA Bosio A., Binczek E., Lebeau M.M., Fernald A.A., Stoffel W.;
RT "The human gene CGT encoding the UDP-galactose ceramide galactosyl
RT transferase (cerebroside synthase): cloning, characterization, and
RT assignment to human chromosome 4, band q26.";
RN Genomics 34:69-75(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97242209; PubMed=9125199;
RA Kapitonov D.E., Yu R.K.;
RT "Cloning, characterization, and expression of human ceramide
RT galactosyltransferase cDNA.";
RL Biochem. Biophys. Res. Commun. 232:449-453(1997).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY
ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: UDP-GALACTOSE + 2-(2-HYDROXYACETYL)SPHINGOSINE
= UDP + 1-(BETA-D-GALACTOSYL)-2-(2-HYDROXYACETYL)SPHINGOSINE.
CC -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDE.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U30930; AAC50565.1; -.
DR EMBL: U32370; AAC50815.1; -.
DR EMBL: U31353; AAC50815.1; JOINED.
DR EMBL: U31461; AAC50815.1; JOINED.
DR EMBL: U31658; AAC50815.1; JOINED.

```

This SWISSPORT entry is copyright © It is produced through a collaboration between the Swiss Institute of Bioinformatics and The EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way used to promote or endorse any product or service. This statement is not removed, Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/isb-sib.ch>) or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC-1- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE. A KEY  
J. Neurosci. Res. 38:234-242(1994).  
RT encode rat UDP-galactose:ceramide galactosyltransferase".  
RT "Isolation, characterization, and expression of cDNA clones that  
RT RT  
CC

```

CC      ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
CC      ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
CC      NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC      -1- CATALYTIC ACTIVITY: UDP-GALACTOSE + 2-(2-HYDROXYACYL)SPHINGOSINE
CC      = UDP + 1-(BETA-D-GALACTOSYL)-2-(2-HYDROXYACYL)SPHINGOSINE.
CC      -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDE.
CC      -1- TISSUE SPECIFICITY: BRAIN, RESTRICTED TO THE OLIGODENDROCYTE-
CC      CONTAINING CELL LAYERS OF CEREBRUM AND CEREBELLUM.
CC      -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L21698; AAA16108.1; -.
DR      EMBL; U07683; AAA50212.1; -.
DR      InterPro; IPR002213; -.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW      Microsome.
FT      SIGNAL      1      20      POTENTIAL.
FT      CHAIN      21      541      2-HYDROXYACYLSPHINGOSINE 1-BETA-
FT      TRANSMEM      472      492      GALACTOSYLTRANSFERASE.
FT      CARBOHYD      78      78      POTENTIAL.
FT      CARBOHYD      333      333      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      442      442      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      SEQUENCE      541 AA; 61126 MW; 260D7603170151BB CRC64;
OY      356 PONDILGH 363
DB      342 PONDILGH 349

```

Search completed: August 13, 2001, 13:47:23  
 Job time: 198 sec

THIS PAGE BLANK (USPTO)